

SEQUENCE LISTING

<110> Alitalo et al

<120> VEGF-C OR VEGF-D MATERIALS AND METHODS FOR OLIGODENDROCYTES

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<170> PatentIn version 3.0

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 Gln Ile Val Phe Glu Gly Val Ile Gly Lys Gly Arg Ser Gly Glu Ile
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gcc att gat gac att cgg ata agc act gat gtc cca ctg gag aac tgc 2400
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 785 790 795 800

atg gaa ccc atc tcg gct ttt gca gtg gac atc cca gaa ata cat gag 2448
 Met Glu Pro Ile Ser Ala Phe Ala Val Asp Ile Pro Glu Ile His Glu
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 Leu Leu Leu Tyr Cys Thr Cys Ser Tyr Ser Gly Leu Ser Ser Arg Ser
 885 890 895

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 Cys Thr Thr Leu Glu Asn Tyr Asn Phe Glu Leu Tyr Asp Gly Leu Lys
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Tyr Pro Ser His Gln Asn Cys Glu Trp Ile Val Tyr Ala Pro Glu Pro
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Asn Gln Lys Ile Val Leu Asn Phe Asn Pro His Phe Glu Ile Glu Lys
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His Asp Cys Lys Tyr Asp Phe Ile Glu Ile Arg Asp Gly Asp Ser Glu
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Gly Ser Glu Asp Cys Ser Lys Asn Phe Thr Ser Pro Asn Gly Thr Ile
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Glu Ser Pro Gly Phe Pro Glu Lys Tyr Pro His Asn Leu Asp Cys Thr
 165 170 175

Phe Thr Ile Leu Ala Lys Pro Lys Met Glu Ile Ile Leu Gln Phe Leu
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Ile Phe Asp Leu Glu His Asp Pro Leu Gln Val Gly Glu Gly Asp Cys
 195 200 205

Lys Tyr Asp Trp Leu Asp Ile Trp Asp Gly Ile Pro His Val Gly Pro
 210 215 220

Leu Ile Gly Lys Tyr Cys Gly Thr Lys Thr Pro Ser Glu Leu Arg Ser
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Ser Thr Gly Ile Leu Ser Leu Thr Phe His Thr Asp Met Ala Val Ala
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Lys Asp Gly Phe Ser Ala Arg Tyr Tyr Leu Val His Gln Glu Pro Leu
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Glu Asn Phe Gln Cys Asn Val Pro Leu Gly Met Glu Ser Gly Arg Ile
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Ala Asn Glu Gln Ile Ser Ala Ser Ser Thr Tyr Ser Asp Gly Arg Trp
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Thr Pro Gln Gln Ser Arg Leu His Gly Asp Asp Asn Gly Trp Thr Pro
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 Asn Leu Asp Ser Asn Lys Glu Tyr Leu Gln Val Asp Leu Arg Phe Leu
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 Gly Glu Asp Trp Met Val Tyr Arg His Gly Lys Asn His Lys Val Phe
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 Pro Leu Leu Thr Arg Phe Val Arg Ile Arg Pro Gln Thr Trp His Ser
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 Thr Val Lys Gly Val Ile Ile Gln Gly Ala Arg Gly Gly Asp Ser Ile
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Lys Ser Glu Glu Thr Thr Thr Pro Tyr Pro Thr Glu Glu Glu Ala Thr
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Glu Cys Gly Glu Asn Cys Ser Phe Glu Asp Asp Lys Asp Leu Gln Leu
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Pro Ser Gly Phe Asn Cys Asn Phe Asp Phe Leu Glu Glu Pro Cys Gly
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Trp Met Tyr Asp His Ala Lys Trp Leu Arg Thr Thr Trp Ala Ser Ser
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Ser Ser Pro Asn Asp Arg Thr Phe Pro Asp Asp Arg Asn Phe Leu Arg
 675 685

Leu Gln Ser Asp Ser Gln Arg Glu Gly Gln Tyr Ala Arg Leu Ile Ser
 690 695 700

Pro Pro Val His Leu Pro Arg Ser Pro Val Cys Met Glu Phe Gln Tyr
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Gln Ala Thr Gly Gly Arg Gly Val Ala Leu Gln Val Val Arg Glu Ala
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Ser Gln Glu Ser Lys Leu Leu Trp Val Ile Arg Glu Asp Gln Gly Gly
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Glu Trp Lys His Gly Arg Ile Ile Leu Pro Ser Tyr Asp Met Glu Tyr
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Gln Ile Val Phe Glu Gly Val Ile Gly Lys Gly Arg Ser Gly Glu Ile
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Ala Ile Asp Asp Ile Arg Ile Ser Thr Asp Val Pro Leu Glu Asn Cys
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Met Glu Pro Ile Ser Ala Phe Ala Val Asp Ile Pro Glu Ile His Glu
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Arg Glu Gly Tyr Glu Asp Glu Ile Asp Asp Glu Tyr Glu Val Asp Trp
820 825 830

Ser Asn Ser Ser Ser Ala Thr Ser Gly Ser Gly Ala Pro Ser Thr Asp
835 840 845

Lys Glu Lys Ser Trp Leu Tyr Thr Leu Asp Pro Ile Leu Ile Thr Ile
850 855 860

Ile Ala Met Ser Ser Leu Gly Val Leu Leu Gly Ala Thr Cys Ala Gly
865 870 875 880

Leu Leu Leu Tyr Cys Thr Cys Ser Tyr Ser Gly Leu Ser Ser Arg Ser
885 890 895

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Met Glu Arg
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Gly Leu Pro Leu Leu Cys Ala Thr Leu Ala Leu Ala Leu Ala
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gag aag tgt gaa tgg cta atc caa gct ccg gaa ccc tac cag aga atc Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Glu Pro Tyr Gln Arg Ile 55 60 65	548
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cct gaa aaa tac ccc aac tgc ttg gag tgc acc tac atc atc ttt gca Pro Glu Lys Tyr Pro Asn Cys Leu Glu Cys Thr Tyr Ile Ile Phe Ala 165 170 175	884
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tgt ggg cag aaa act cct ggc cgg atc cgc tcc tct tca ggc gtt cta Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser Gly Val Leu 230 235 240	1076
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 Lys Thr Tyr Arg Val Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Ser 370
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 Val Arg Ile Lys Pro Val Ser Trp Glu Thr Gly Ile Ser Met Arg Phe 415
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 Ile Gln Gly Gly Lys His Arg Glu Asn Lys Val Phe Met Arg Lys Phe 515
 500 505 510

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 Lys Ile Ala Tyr Ser Asn Asn Gly Ser Asp Trp Lys Thr Ile Met Asp 530
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 Pro Gln Ser Asn Tyr Ser Glu Ala
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His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Glu Pro Tyr
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Gln Arg Ile Ile Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg
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Asp Cys Lys Tyr Asp Tyr Val Glu Val Ile Asp Gly Glu Asn Glu Gly
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Gly Arg Leu Trp Gly Lys Phe Cys Gly Lys Ile Ala Pro Ser Pro Val
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Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu
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Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly
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Asp Leu Glu Gln Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr
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Gly Val Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu
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Thr Thr Pro Asn Gly Asn Pro Val His Glu Cys Asp Asp Asp Gln Ala
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Ser Glu Phe Pro Thr Tyr Gly Phe Asn Cys Glu Phe Gly Trp Gly Ser
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His Lys Thr Phe Cys His Trp Glu His Asp Ser His Ala Gln Leu Arg
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Asp Gly Asn Phe Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys Gly Lys
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Ile Gly Lys Gly Asn Leu Gly Gly Ile Ala Val Asp Asp Ile Ser Ile
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Lys Lys Asn Thr Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr Pro Gly
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Tyr Glu Gly Glu Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys Pro Gly
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Asn Val Leu Lys Thr Leu Asp Pro Ile Leu Ile Thr Ile Ile Ala Met
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aac att ttc aag gga tca gcc gtg tgt atg tat agc atg agt gat gtg Asn Ile Phe Lys Gly Ser Ala Val Cys Met Tyr Ser Met Ser Asp Val 335 340 345	1059
aga agg gtg ttc ctt ggt cca tat gcc cac agg gat gga ccc aac tat Arg Arg Val Phe Leu Gly Pro Tyr Ala His Arg Asp Gly Pro Asn Tyr 350 355 360	1107

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Gln Trp Val Pro Tyr Gln Gly Arg Val Pro Tyr Pro Arg Pro Gly Thr	
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Cys Pro Ser Lys Thr Phe Gly Gly Phe Asp Ser Thr Lys Asp Leu Pro	
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gat gat gtt ata acc ttt gca aga agt cat cca gcc atg tac aat cca	1251
Asp Asp Val Ile Thr Phe Ala Arg Ser His Pro Ala Met Tyr Asn Pro	
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Val Phe Pro Met Asn Asn Arg Pro Ile Val Ile Lys Thr Asp Val Asn	
415 420 425	
tat caa ttt aca caa att gtc gta gac cga gtg gat gca gaa gat gga	1347
Tyr Gln Phe Thr Gln Ile Val Val Asp Arg Val Asp Ala Glu Asp Gly	
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Gln Tyr Asp Val Met Phe Ile Gly Thr Asp Val Gly Thr Val Leu Lys	
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Val Val Ser Ile Pro Lys Glu Thr Trp Tyr Asp Leu Glu Glu Val Leu	
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Leu Glu Glu Met Thr Val Phe Arg Glu Pro Thr Ala Ile Ser Ala Met	
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gag ctt tcc act aag cag caa caa cta tat att ggt tca acg gct ggg	1539
Glu Leu Ser Thr Lys Gln Gln Gln Leu Tyr Ile Gly Ser Thr Ala Gly	
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gtt gcc cag ctc cct tta cac cgg tgt gat att tac ggg aaa gcg tgt	1587
Val Ala Gln Leu Pro Leu His Arg Cys Asp Ile Tyr Gly Lys Ala Cys	
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Ala Glu Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ser	
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Ala Cys Ser Arg Tyr Phe Pro Thr Ala Lys Arg Arg Thr Arg Arg Gln	
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Asp Ile Arg Asn Gly Asp Pro Leu Thr His Cys Ser Asp Leu His His	
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Asp Asn His His Gly His Ser Pro Glu Glu Arg Ile Ile Tyr Gly Val	
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Glu Asn Ser Ser Thr Phe Leu Glu Cys Ser Pro Lys Ser Gln Arg Ala	
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Leu Val Tyr Trp Gln Phe Gln Arg Arg Asn Glu Glu Arg Lys Glu Glu	
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 Ile Arg Val Asp Asp His Ile Ile Arg Thr Asp Gln Gly Leu Leu Leu
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cgt agt cta caa cag aag gat tca ggc aat tac ctc tgc cat gcg gtg 1971
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gaa cat ggg ttc ata caa act ctt ctt aag gta acc ctg gaa gtc att 2019
 Glu His Gly Phe Ile Gln Thr Leu Leu Lys Val Thr Leu Glu Val Ile
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gac aca gag cat ttg gaa gaa ctt ctt cat aaa gat gat gat gga gat 2067
 Asp Thr Glu His Leu Glu Glu Leu Leu His Lys Asp Asp Asp Gly Asp
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ggc tct aag acc aaa gaa atg tcc aat agc atg aca cct agc cag aag 2115
 Gly Ser Lys Thr Lys Glu Met Ser Asn Ser Met Thr Pro Ser Gln Lys
 685 690 695 700

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 Val Trp Tyr Arg Asp Phe Met Gln Leu Ile Asn His Pro Asn Leu Asn
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acg atg gat gag ttc tgt gaa caa gtt tgg aaa agg gac cga aaa caa 2211
 Thr Met Asp Glu Phe Cys Glu Gln Val Trp Lys Arg Asp Arg Lys Gln
 720 725 730

cgt cgg caa agg cca gga cat acc cca ggg aac agt aac aaa tgg aag 2259
 Arg Arg Gln Arg Pro Gly His Thr Pro Gly Asn Ser Asn Lys Trp Lys
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cac tta caa gaa aat aag aaa ggt aga aac agg agg acc cac gaa ttt 2307
 His Leu Gln Glu Asn Lys Lys Gly Arg Asn Arg Arg Thr His Glu Phe
 750 755 760

gag agg gca ccc agg agt gtc tga gctgcattac ctctagaaac ctcaaacaag 2361
 Glu Arg Ala Pro Arg Ser Val
 765 770

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Lys Leu Ser Tyr Lys Glu Met Leu Glu Ser Asn Asn Val Ile Thr Phe
 35 40 45

Asn Gly Leu Ala Asn Ser Ser Ser Tyr His Thr Phe Leu Leu Asp Glu
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Glu Arg Ser Arg Leu Tyr Val Gly Ala Lys Asp His Ile Phe Ser Phe
 65 70 75 80

Asp Leu Val Asn Ile Lys Asp Phe Gln Lys Ile Val Trp Pro Val Ser
 85 90 95

Tyr Thr Arg Arg Asp Glu Cys Lys Trp Ala Gly Lys Asp Ile Leu Lys
 100 105 110

Glu Cys Ala Asn Phe Ile Lys Val Leu Lys Ala Tyr Asn Gln Thr His
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Leu Tyr Ala Cys Gly Thr Gly Ala Phe His Pro Ile Cys Thr Tyr Ile
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Glu Ile Gly His His Pro Glu Asp Asn Ile Phe Lys Leu Glu Asn Ser
 145 150 155 160

His Phe Glu Asn Gly Arg Gly Lys Ser Pro Tyr Asp Pro Lys Leu Leu
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Thr Ala Ser Leu Leu Ile Asp Gly Glu Leu Tyr Ser Gly Thr Ala Ala
 180 185 190

Asp Phe Met Gly Arg Asp Phe Ala Ile Phe Arg Thr Leu Gly His His
 195 200 205

His Pro Ile Arg Thr Glu Gln His Asp Ser Arg Trp Leu Asn Asp Pro
 210 215 220

Lys Phe Ile Ser Ala His Leu Ile Ser Glu Ser Asp Asn Pro Glu Asp
 225 230 235 240

Asp Lys Val Tyr Phe Phe Phe Arg Glu Asn Ala Ile Asp Gly Glu His
 245 250 255

Ser Gly Lys Ala Thr His Ala Arg Ile Gly Gln Ile Cys Lys Asn Asp
 260 265 270

Phe Gly Gly His Arg Ser Leu Val Asn Lys Trp Thr Thr Phe Leu Lys
 275 280 285

Ala Arg Leu Ile Cys Ser Val Pro Gly Pro Asn Gly Ile Asp Thr His
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Phe Asp Glu Leu Gln Asp Val Phe Leu Met Asn Phe Lys Asp Pro Lys
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Asn Pro Val Val Tyr Gly Val Phe Thr Thr Ser Ser Asn Ile Phe Lys
 325 330 335

Gly Ser Ala Val Cys Met Tyr Ser Met Ser Asp Val Arg Arg Val Phe
 340 345 350

Leu Gly Pro Tyr Ala His Arg Asp Gly Pro Asn Tyr Gln Trp Val Pro
 355 360 365

Tyr Gln Gly Arg Val Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys
 370 375 380

Thr Phe Gly Gly Phe Asp Ser Thr Lys Asp Leu Pro Asp Asp Val Ile
 385 390 395 400

Thr Phe Ala Arg Ser His Pro Ala Met Tyr Asn Pro Val Phe Pro Met
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Asn Asn Arg Pro Ile Val Ile Lys Thr Asp Val Asn Tyr Gln Phe Thr
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Gln Ile Val Val Asp Arg Val Asp Ala Glu Asp Gly Gln Tyr Asp Val
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Met Phe Ile Gly Thr Asp Val Gly Thr Val Leu Lys Val Val Ser Ile
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Pro Lys Glu Thr Trp Tyr Asp Leu Glu Glu Val Leu Leu Glu Glu Met
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Thr Val Phe Arg Glu Pro Thr Ala Ile Ser Ala Met Glu Leu Ser Thr
 485 490 495

Lys Gln Gln Gln Leu Tyr Ile Gly Ser Thr Ala Gly Val Ala Gln Leu
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Pro Leu His Arg Cys Asp Ile Tyr Gly Lys Ala Cys Ala Glu Cys Cys
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Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ser Ala Cys Ser Arg
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Tyr Phe Pro Thr Ala Lys Arg Arg Thr Arg Arg Gln Asp Ile Arg Asn
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Gly Asp Pro Leu Thr His Cys Ser Asp Leu His His Asp Asn His His
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Gly His Ser Pro Glu Glu Arg Ile Ile Tyr Gly Val Glu Asn Ser Ser
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Thr Phe Leu Glu Cys Ser Pro Lys Ser Gln Arg Ala Leu Val Tyr Trp
 595 600 605

Gln Phe Gln Arg Arg Asn Glu Glu Arg Lys Glu Glu Ile Arg Val Asp
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Asp His Ile Ile Arg Thr Asp Gln Gly Leu Leu Leu Arg Ser Leu Gln
 625 630 635 640

Gln Lys Asp Ser Gly Asn Tyr Leu Cys His Ala Val Glu His Gly Phe
 645 650 655

Ile Gln Thr Leu Leu Lys Val Thr Leu Glu Val Ile Asp Thr Glu His
 660 665 670

Leu Glu Glu Leu Leu His Lys Asp Asp Asp Gly Asp Gly Ser Lys Thr
 675 680 685

Lys Glu Met Ser Asn Ser Met Thr Pro Ser Gln Lys Val Trp Tyr Arg
 690 695 700

Asp Phe Met Gln Leu Ile Asn His Pro Asn Leu Asn Thr Met Asp Glu
 705 710 715 720

Phe Cys Glu Gln Val Trp Lys Arg Asp Arg Lys Gln Arg Arg Gln Arg
 725 730 735

Pro Gly His Thr Pro Gly Asn Ser Asn Lys Trp Lys His Leu Gln Glu
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Arg Ser Val
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 Met
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 ggg cgg gcc ggg gct gcc gcc gtg atc ccg ggc ctg gcc ctg ctc tgg 286
 Gly Arg Ala Gly Ala Ala Ala Val Ile Pro Gly Leu Ala Leu Leu Trp
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 gca gtg ggg ctg ggg agt gcc gcc ccc agc ccc cca cgc ctt cgg ctc 334
 Ala Val Gly Leu Gly Ser Ala Ala Pro Ser Pro Pro Arg Leu Arg Leu
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 Ser Phe Gln Glu Leu Gln Ala Trp His Gly Leu Gln Thr Phe Ser Leu
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 Glu Arg Thr Cys Cys Tyr Gln Ala Leu Leu Val Asp Glu Glu Arg Gly
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 cgc ctg ttt gtg ggt gcc gag aac cat gtg gcc tcc ctc aac ctg gac 478
 Arg Leu Phe Val Gly Ala Glu Asn His Val Ala Ser Leu Asn Leu Asp
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 aac atc agc aag cgg gcc aag aag ctg gcc tgg ccg gcc cct gtg gaa 526
 Asn Ile Ser Lys Arg Ala Lys Lys Leu Ala Trp Pro Ala Pro Val Glu
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 tgg cga gag gag tgc aac tgg gca ggg aag gac att ggt act gag tgc 574
 Trp Arg Glu Glu Cys Asn Trp Ala Gly Lys Asp Ile Gly Thr Glu Cys
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 atg aac ttc gtg aag ttg ctg cat gcc tac aac cgc acc cat ttg ctg 622
 Met Asn Phe Val Lys Leu Leu His Ala Tyr Asn Arg Thr His Leu Leu
 115 120 125
 gcc tgt ggc acg gga gcc ttc cac cca acc tgt gcc ttt gtg gaa gtg 670
 Ala Cys Gly Thr Gly Ala Phe His Pro Thr Cys Ala Phe Val Glu Val
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 ggc cac cgg gca gag gag ccc gtc ctc cgg ctg gac cca gga agg ata 718
 Gly His Arg Ala Glu Glu Pro Val Leu Arg Leu Asp Pro Gly Arg Ile
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 gag gat ggc aag ggg aag agt cct tat gac ccc agg cat cgg gct gcc 766
 Glu Asp Gly Lys Gly Lys Ser Pro Tyr Asp Pro Arg His Arg Ala Ala
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gcg cgg aac cac ccc ctc atg tac aac tct gtc ctg ccc act ggg ggg Ala Arg Asn His Pro Leu Met Tyr Asn Ser Val Leu Pro Thr Gly Gly 405 410 415	1486
cgc cct ctt ttc cta caa gtt gga gcc aat tac acc ttc act caa att Arg Pro Leu Phe Leu Gln Val Gly Ala Asn Tyr Thr Phe Thr Gln Ile 420 425 430	1534

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Ile	Gly	Thr	Asp	Val	Gly	Thr	Val	Leu	Lys	Val	Ile	Ser	Val	Pro	Lys	
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Gly	Ser	Arg	Pro	Ser	Ala	Glu	Gly	Leu	Leu	Leu	Glu	Glu	Leu	His	Val	
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ttt	gag	gac	tcg	gcc	gct	gtc	acc	agc	atg	caa	att	tct	tcc	aag	agg	1726
Phe	Glu	Asp	Ser	Ala	Ala	Val	Thr	Ser	Met	Gln	Ile	Ser	Ser	Lys	Arg	
			485					490					495			
cac	cag	ctg	tac	gta	gcc	tcg	cgg	agc	gcg	gtg	gcc	cag	atc	gcg	ttg	1774
His	Gln	Leu	Tyr	Val	Ala	Ser	Arg	Ser	Ala	Val	Ala	Gln	Ile	Ala	Leu	
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cac	cgc	tgc	gct	gcc	cac	ggc	cgc	gtc	tgc	acc	gaa	tgc	tgt	ctg	gcg	1822
His	Arg	Cys	Ala	Ala	His	Gly	Arg	Val	Cys	Thr	Glu	Cys	Cys	Leu	Ala	
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cgt	gac	ccc	tac	tgc	gcc	tgg	gac	ggg	gtc	gcg	tgc	acg	cgc	ttc	cag	1870
Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp	Gly	Val	Ala	Cys	Thr	Arg	Phe	Gln	
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Pro	Ser	Ala	Lys	Arg	Arg	Phe	Arg	Arg	Gln	Asp	Val	Arg	Asn	Gly	Asp	
				550					555					560		
ccc	agc	acg	ttg	tgc	tcc	gga	gac	tcg	tct	cgt	ccc	gcg	ctg	ctg	gaa	1966
Pro	Ser	Thr	Leu	Cys	Ser	Gly	Asp	Ser	Ser	Arg	Pro	Ala	Leu	Leu	Glu	
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Pro	Arg	Ser	Leu	Gln	Ala	Arg	Val	Glu	Trp	Thr	Phe	Gln	Arg	Ala	Gly	
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Tyr	Leu	Cys	Ala	Ala	Val	Glu	Gln	Gly	Phe	Thr	Gln	Pro	Leu	Arg	Arg	
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Leu	Ser	Leu	His	Val	Leu	Ser	Ala	Thr	Gln	Ala	Glu	Arg	Leu	Ala	Arg	
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 740 745

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Leu Glu Arg Thr Cys Cys Tyr Gln Ala Leu Leu Val Asp Glu Glu Arg
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Gly Arg Leu Phe Val Gly Ala Glu Asn His Val Ala Ser Leu Asn Leu
 65 70 75 80

Asp Asn Ile Ser Lys Arg Ala Lys Lys Leu Ala Trp Pro Ala Pro Val
 85 90 95

Glu Trp Arg Glu Glu Cys Asn Trp Ala Gly Lys Asp Ile Gly Thr Glu
 100 105 110

Cys Met Asn Phe Val Lys Leu Leu His Ala Tyr Asn Arg Thr His Leu
 115 120 125

Leu Ala Cys Gly Thr Gly Ala Phe His Pro Thr Cys Ala Phe Val Glu
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Val Gly His Arg Ala Glu Glu Pro Val Leu Arg Leu Asp Pro Gly Arg
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Ile Glu Asp Gly Lys Gly Lys Ser Pro Tyr Asp Pro Arg His Arg Ala
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Ala Ser Val Leu Val Gly Glu Glu Leu Tyr Ser Gly Val Ala Ala Asp
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Lys Ile Tyr Phe Phe Phe Arg Glu Thr Ala Val Glu Ala Ala Pro Ala
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Phe Gly Thr Phe Ser Ser Thr Lys Asp Phe Pro Asp Asp Val Ile Gln
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Ile Ala Ala Asp Arg Val Ala Ala Ala Asp Gly His Tyr Asp Val Leu
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Val Phe Glu Asp Ser Ala Ala Val Thr Ser Met Gln Ile Ser Ser Lys
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Leu His Arg Cys Ala Ala His Gly Arg Val Cys Thr Glu Cys Cys Leu
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Gln Pro Ser Ala Lys Arg Arg Phe Arg Arg Gln Asp Val Arg Asn Gly
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Asp Pro Ser Thr Leu Cys Ser Gly Asp Ser Ser Arg Pro Ala Leu Leu
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Glu His Lys Val Phe Gly Val Glu Gly Ser Ser Ala Phe Leu Glu Cys
 580 585 590

Glu Pro Arg Ser Leu Gln Ala Arg Val Glu Trp Thr Phe Gln Arg Ala
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Gly Val Thr Ala His Thr Gln Val Leu Ala Glu Glu Arg Thr Glu Arg
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Thr Ala Arg Gly Leu Leu Leu Arg Arg Leu Arg Arg Arg Asp Ser Gly
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Val Tyr Leu Cys Ala Ala Val Glu Gln Gly Phe Thr Gln Pro Leu Arg
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Arg Leu Ser Leu His Val Leu Ser Ala Thr Gln Ala Glu Arg Leu Ala
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Arg Ala Glu Glu Ala Ala Pro Ala Ala Pro Pro Gly Pro Lys Leu Trp
675 680 685

Tyr Arg Asp Phe Leu Gln Leu Val Glu Pro Gly Gly Gly Gly Ser Ala
690 695 700

Asn Ser Leu Arg Met Cys Arg Pro Gln Pro Ala Leu Gln Ser Leu Pro
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Thr Val Phe Asn Gly Pro Phe Ala His Lys Glu Gly Pro Asn His Gln	
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Ile Tyr Pro Ile His Lys Arg Pro Leu Ile Val Arg Ile Gly Thr Asp	
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Gly Thr Asp Ala Ala Ile Phe Arg Ser Leu Thr Lys Arg Asn Ala Val
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Leu Gly Thr Asp Arg Gly Thr Val Gln Lys Val Val Val Leu Pro Thr
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Ser Gln Gly Leu Leu Ile Arg Ser Val Gln Gly Ser Asp Gln Gly Leu
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Tyr His Cys Ile Ala Thr Glu Asn Ser Phe Lys Gln Thr Ile Ala Lys
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Ile Asn Phe Lys Val Leu Asp Ser Glu Met Val Ala Val Val Thr Asp
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Lys Trp Ser Pro Trp Thr Trp Ala Ser Ser Val Arg Ala Leu Pro Phe
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His Pro Lys Asp Ile Met Gly Ala Phe Ser His Ser Glu Met Gln Met
690 695 700

Ile Asn Gln Tyr Cys Lys Asp Thr Arg Gln Gln His Gln Gln Gly Asp
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acc atc tct tct aag agg caa caa ctc tac gtg gcg tca gcc gtg ggt Thr Ile Ser Ser Lys Arg Gln Gln Leu Tyr Val Ala Ser Ala Val Gly 525 530 535	1695
gtc aca cac ctg agc ctg cac cgc tgc cag gcg tat ggg gct gcc tgt Val Thr His Leu Ser Leu His Arg Cys Gln Ala Tyr Gly Ala Ala Cys 540 545 550 555	1743
gct gac tgc tgc ctt gcc cgg gac cct tac tgt gcc tgg gat ggc cag Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Gln 560 565 570	1791
gcc tgc tcc cgc tat aca gca tcc tcc aag agg cgg agc cgc cgg cag Ala Cys Ser Arg Tyr Thr Ala Ser Ser Lys Arg Arg Ser Arg Arg Gln 575 580 585	1839
gac gtc cgg cac gga aac ccc atc agg cag tgc cgt ggg ttc aac tcc Asp Val Arg His Gly Asn Pro Ile Arg Gln Cys Arg Gly Phe Asn Ser 590 595 600	1887
aat gcc aac aag aat gcc gtg gag tct gtg cag tat ggc gtg gcc ggc Asn Ala Asn Lys Asn Ala Val Glu Ser Val Gln Tyr Gly Val Ala Gly 605 610 615	1935
agc gca gcc ttc ctt gag tgc cag ccc cgc tgc ccc caa gcc act gtt Ser Ala Ala Phe Leu Glu Cys Gln Pro Arg Ser Pro Gln Ala Thr Val 620 625 630 635	1983
aag tgg ctg ttc cag cga gat cct ggt gac cgg cgc cga gag att cgt Lys Trp Leu Phe Gln Arg Asp Pro Gly Asp Arg Arg Arg Glu Ile Arg 640 645 650	2031
gca gag gac cgc ttc ctg cgc aca gag cag ggc ttg ttg ctc cgt gca Ala Glu Asp Arg Phe Leu Arg Thr Glu Gln Gly Leu Leu Arg Ala 655 660 665	2079
ctg cag ctc agc gat cgt ggc ctc tac tcc tgc aca gcc act gag aac Leu Gln Leu Ser Asp Arg Gly Leu Tyr Ser Cys Thr Ala Thr Glu Asn 670 675 680	2127
aac ttt aag cac gtc gtc aca cga gtg cag ctg cat gta ctg ggc cgg Asn Phe Lys His Val Val Thr Arg Val Gln Leu His Val Leu Gly Arg 685 690 695	2175

gac gcc gtc cat gct gcc ctg ttc cca cca ctg tcc atg agc gcc ccg 2223
 Asp Ala Val His Ala Ala Leu Phe Pro Pro Leu Ser Met Ser Ala Pro
 700 705 710 715

cca ccc cca ggc gca ggc ccc cca acg cct cct tac cag gag tta gcc 2271
 Pro Pro Pro Gly Ala Gly Pro Pro Thr Pro Pro Tyr Gln Glu Leu Ala
 720 725 730

cag ctg ctg gcc cag cca gaa gtg ggc ctg atc cac cag tac tgc cag 2319
 Gln Leu Leu Ala Gln Pro Glu Val Gly Leu Ile His Gln Tyr Cys Gln
 735 740 745

ggt tac tgg cgc cat gtg ccc ccc agc ccc agg gag gct cca ggg gca 2367
 Gly Tyr Trp Arg His Val Pro Pro Ser Pro Arg Glu Ala Pro Gly Ala
 750 755 760

ccc cgg tct cct gag ccc cag gac cag aaa aag ccc cgg aac cgc cgg 2415
 Pro Arg Ser Pro Glu Pro Gln Asp Gln Lys Lys Pro Arg Asn Arg Arg
 765 770 775

cac cac cct ccg gac aca tga ggccagctgc ctgtgcctgc catgggccag 2466
 His His Pro Pro Asp Thr
 780 785

gctaggcctt ggtccctttt aatataaaag atatatatat atatatatat atatattaaa 2526
 atatcgggggt ggggggtgat tggaaggag ggaggtggcc ttcccaatgc gcgttattcg 2586
 gggttattga agaataatat tgcaagtgc agccagaagt agactttctg tcctcacacc 2646
 gaagaacccg agtgagcagg agggagggag agacgcgaag agaccttttt tcctttttgg 2706
 agaccttgtc cgc 2719

<210> 18
 <211> 785
 <212> PRT
 <213> Homo sapiens

<400> 18

Met Leu Val Ala Gly Leu Leu Leu Trp Ala Ser Leu Leu Thr Gly Ala
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Trp Pro Ser Phe Pro Thr Gln Asp His Leu Pro Ala Thr Pro Arg Val
 20 25 30

Arg Leu Ser Phe Lys Glu Leu Lys Ala Thr Gly Thr Ala His Phe Phe
 35 40 45

Asn Phe Leu Leu Asn Thr Thr Asp Tyr Arg Ile Leu Leu Lys Asp Glu
 50 55 60

Asp His Asp Arg Met Tyr Val Gly Ser Lys Asp Tyr Val Leu Ser Leu
 65 70 75 80

Asp Leu His Asp Ile Asn Arg Glu Pro Leu Ile Ile His Trp Ala Ala
 85 90 95

Ser Pro Gln Arg Ile Glu Glu Cys Val Leu Ser Gly Lys Asp Val Asn
 100 105 110

Gly Glu Cys Gly Asn Phe Val Arg Leu Ile Gln Pro Trp Asn Arg Thr
 115 120 125

His Leu Tyr Val Cys Gly Thr Gly Ala Tyr Asn Pro Met Cys Thr Tyr
 130 135 140

Val Asn Arg Gly Arg Arg Ala Gln Ala Thr Pro Trp Thr Gln Thr Gln
 145 150 155 160

Ala Val Arg Gly Arg Gly Ser Arg Ala Thr Asp Gly Ala Leu Arg Pro
 165 170 175

Met Pro Thr Ala Pro Arg Gln Asp Tyr Ile Phe Tyr Leu Glu Pro Glu
 180 185 190

Arg Leu Glu Ser Gly Lys Gly Lys Cys Pro Tyr Asp Pro Lys Leu Asp
 195 200 205

Thr Ala Ser Ala Leu Ile Asn Glu Glu Leu Tyr Ala Gly Val Tyr Ile
 210 215 220

Asp Phe Met Gly Thr Asp Ala Ala Ile Phe Arg Thr Leu Gly Lys Gln
 225 230 235 240

Thr Ala Met Arg Thr Asp Gln Tyr Asn Ser Arg Trp Leu Asn Asp Pro
 245 250 255

Ser Phe Ile His Ala Glu Leu Ile Pro Asp Ser Ala Glu Arg Asn Asp
 260 265 270

Asp Lys Leu Tyr Phe Phe Phe Arg Glu Arg Ser Ala Glu Ala Pro Gln
 275 280 285

Ser Pro Ala Val Tyr Ala Arg Ile Gly Arg Ile Cys Leu Asn Asp Asp
 290 295 300

Gly Gly His Cys Cys Leu Val Asn Lys Trp Ser Thr Phe Leu Lys Ala
 305 310 315 320

Arg Leu Val Cys Ser Val Pro Gly Glu Asp Gly Ile Glu Thr His Phe
 325 330 335

Asp Glu Leu Gln Asp Val Phe Val Gln Gln Thr Gln Asp Val Arg Asn
 340 345 350

Pro Val Ile Tyr Ala Val Phe Thr Ser Ser Gly Ser Val Phe Arg Gly
 355 360 365

Ser Ala Val Cys Val Tyr Ser Met Ala Asp Ile Arg Met Val Phe Asn
 370 375 380

Gly Pro Phe Ala His Lys Glu Gly Pro Asn Tyr Gln Trp Met Pro Phe
 385 390 395 400

Ser Gly Lys Met Pro Tyr Pro Arg Pro Gly Thr Cys Pro Gly Gly Thr
 405 410 415

Phe Thr Pro Ser Met Lys Ser Thr Lys Asp Tyr Pro Asp Glu Val Ile
 420 425 430

Asn Phe Met Arg Ser His Pro Leu Met Tyr Gln Ala Val Tyr Pro Leu
 435 440 445

Gln Arg Arg Pro Leu Val Val Arg Thr Gly Ala Pro Tyr Arg Leu Thr
 450 455 460

Thr Ile Ala Val Asp Gln Val Asp Ala Gly Asp Gly Arg Tyr Glu Val
 465 470 475 480

Leu Phe Leu Gly Thr Asp Arg Gly Thr Val Gln Lys Val Ile Val Leu
 485 490 495

Pro Lys Asp Asp Gln Glu Met Glu Glu Leu Met Leu Glu Glu Val Glu
 500 505 510

Val Phe Lys Asp Pro Ala Pro Val Lys Thr Met Thr Ile Ser Ser Lys
 515 520 525

Arg Gln Gln Leu Tyr Val Ala Ser Ala Val Gly Val Thr His Leu Ser
 530 535 540

Leu His Arg Cys Gln Ala Tyr Gly Ala Ala Cys Ala Asp Cys Cys Leu
 545 550 555 560

Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Gln Ala Cys Ser Arg Tyr
 565 570 575

Thr Ala Ser Ser Lys Arg Arg Ser Arg Arg Gln Asp Val Arg His Gly
 580 585 590

Asn Pro Ile Arg Gln Cys Arg Gly Phe Asn Ser Asn Ala Asn Lys Asn
595 600 605

Ala Val Glu Ser Val Gln Tyr Gly Val Ala Gly Ser Ala Ala Phe Leu
610 615 620

Glu Cys Gln Pro Arg Ser Pro Gln Ala Thr Val Lys Trp Leu Phe Gln
625 630 635 640

Arg Asp Pro Gly Asp Arg Arg Arg Glu Ile Arg Ala Glu Asp Arg Phe
645 650 655

Leu Arg Thr Glu Gln Gly Leu Leu Leu Arg Ala Leu Gln Leu Ser Asp
660 665 670

Arg Gly Leu Tyr Ser Cys Thr Ala Thr Glu Asn Asn Phe Lys His Val
675 680 685

Val Thr Arg Val Gln Leu His Val Leu Gly Arg Asp Ala Val His Ala
690 695 700

Ala Leu Phe Pro Pro Leu Ser Met Ser Ala Pro Pro Pro Gly Ala
705 710 715 720

Gly Pro Pro Thr Pro Pro Tyr Gln Glu Leu Ala Gln Leu Leu Ala Gln
725 730 735

Pro Glu Val Gly Leu Ile His Gln Tyr Cys Gln Gly Tyr Trp Arg His
740 745 750

Val Pro Pro Ser Pro Arg Glu Ala Pro Gly Ala Pro Arg Ser Pro Glu
755 760 765

Pro Gln Asp Gln Lys Lys Pro Arg Asn Arg Arg His His Pro Pro Asp
770 775 780

Thr
785

<210> 19
<211> 649
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (17) .. (592)

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<220>
<221> misc_feature
<222> (17)..(94)
<223> Signal peptide

<400> . 19
tcgggcctcc gaaacc atg aac ttt ctg ctg tct tgg gtg cat tgg agc ctt      52
      Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu
            1             5             10

gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc      100
Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
      15             20             25

atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg      148
Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
      30             35             40

gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac      196
Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
      45             50             55

atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc      244
Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
            65             70             75

tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg      292
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
            80             85             90

gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg      340
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
            95             100            105

atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag      388
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
            110            115            120

cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa      436
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
            125            130            135            140

aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa      484
Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
            145            150            155

gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc      532
Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
            160            165            170

aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag      580
Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
            175            180            185

ccg agg cgg tga gccgggcagg aggaaggagc ctccctcagc gtttcgggaa      632
Pro Arg Arg
            190

ccagatctct caccagg      649

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<210> 20
 <211> 191
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (17)..(94)
 <223> Signal peptide

<400> 20

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
 130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
 145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
 165 170 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
 180 185 190

<210> 21
 <211> 755
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (5) .. (628)

<400> 21

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	Met	Ser	Pro	Leu	Leu	Arg	Arg	Leu	Leu	Leu	Ala	Ala	Leu	Leu	Gln	
	1				5					10					15	
ctg	gcc	ccc	gcc	cag	gcc	cct	gtc	tcc	cag	cct	gat	gcc	cct	ggc	cac	97
Leu	Ala	Pro	Ala	Gln	Ala	Pro	Val	Ser	Gln	Pro	Asp	Ala	Pro	Gly	His	
				20					25					30		
cag	agg	aaa	gtg	gtg	tca	tgg	ata	gat	gtg	tat	act	cgc	gct	acc	tgc	145
Gln	Arg	Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	
			35					40					45			
cag	ccc	cgg	gag	gtg	gtg	gtg	ccc	ttg	act	gtg	gag	ctc	atg	ggc	acc	193
Gln	Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	
			50				55						60			
gtg	gcc	aaa	cag	ctg	gtg	ccc	agc	tgc	gtg	act	gtg	cag	cgc	tgt	ggt	241
Val	Ala	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	
	65					70					75					
ggc	tgc	tgc	cct	gac	gat	ggc	ctg	gag	tgt	gtg	ccc	act	ggg	cag	cac	289
Gly	Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	
	80				85					90				95		
caa	gtc	cgg	atg	cag	atc	ctc	atg	atc	cgg	tac	ccg	agc	agt	cag	ctg	337
Gln	Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	
				100					105					110		
ggg	gag	atg	tcc	ctg	gaa	gaa	cac	agc	cag	tgt	gaa	tgc	aga	cct	aaa	385
Gly	Glu	Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	
			115					120					125			
aaa	aag	gac	agt	gct	gtg	aag	cca	gac	agg	gct	gcc	act	ccc	cac	cac	433
Lys	Lys	Asp	Ser	Ala	Val	Lys	Pro	Asp	Arg	Ala	Ala	Thr	Pro	His	His	
		130					135					140				
cgt	ccc	cag	ccc	cgt	tct	gtt	ccg	ggc	tgg	gac	tct	gcc	ccc	gga	gca	481
Arg	Pro	Gln	Pro	Arg	Ser	Val	Pro	Gly	Trp	Asp	Ser	Ala	Pro	Gly	Ala	
	145					150					155					
ccc	tcc	cca	gct	gac	atc	acc	cat	ccc	act	cca	gcc	cca	ggc	ccc	tct	529
Pro	Ser	Pro	Ala	Asp	Ile	Thr	His	Pro	Thr	Pro	Ala	Pro	Gly	Pro	Ser	
	160				165					170					175	
gcc	cac	gct	gca	ccc	agc	acc	acc	agc	gcc	ctg	acc	ccc	gga	cct	gcc	577
Ala	His	Ala	Ala	Pro	Ser	Thr	Thr	Ser	Ala	Leu	Thr	Pro	Gly	Pro	Ala	
				180					185					190		
gcc	gcc	gct	gcc	gac	gcc	gca	gct	tcc	tcc	gtt	gcc	aag	ggc	ggg	gct	625
Ala	Ala	Ala	Ala	Asp	Ala	Ala	Ala	Ser	Ser	Val	Ala	Lys	Gly	Gly	Ala	
			195					200					205			
tag	agctca	accc	agacac	ctgc	aggtgcc	cgga	agctgc	gaag	gtgac	acatg						678
gcttttc	caga	ctcagc	caggg	tgacttgc	ct	cagagg	ctat	atcccag	tgg	gggaaca	aaag					738

aggagcctgg taataaaa

755

<210> 22
 <211> 207
 <212> PRT
 <213> Homo sapiens

<400> 22

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
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Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
 130 135 140

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
 145 150 155 160

Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
 165 170 175

His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
 180 185 190

Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
 195 200 205

[illegible]

gcg aca aac acc ttc ttt aaa cct cca tgt gtg tcc gtc tac aga tgt	837
Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys	
150 155 160	
ggg ggt tgc tgc aat agt gag ggg ctg cag tgc atg aac acc agc acg	885
Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr	
165 170 175	
agc tac ctc agc aag acg tta ttt gaa att aca gtg cct ctc tct caa	933
Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln	
180 185 190	
ggc ccc aaa cca gta aca atc agt ttt gcc aat cac act tcc tgc cga	981
Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg	
195 200 205 210	
tgc atg tct aaa ctg gat gtt tac aga caa gtt cat tcc att att aga	1029
Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg	
215 220 225	
cgt tcc ctg cca gca aca cta cca cag tgt cag gca gcg aac aag acc	1077
Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr	
230 235 240	
tgc ccc acc aat tac atg tgg aat aat cac atc tgc aga tgc ctg gct	1125
Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala	
245 250 255	
cag gaa gat ttt atg ttt tcc tgc gat gct gga gat gac tca aca gat	1173
Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp	
260 265 270	
gga ttc cat gac atc tgt gga cca aac aag gag ctg gat gaa gag acc	1221
Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr	
275 280 285 290	
tgt cag tgt gtc tgc aga gcg ggg ctt cgg cct gcc agc tgt gga ccc	1269
Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro	
295 300 305	
cac aaa gaa cta gac aga aac tca tgc cag tgt gtc tgt aaa aac aaa	1317
His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys	
310 315 320	
ctc ttc ccc agc caa tgt ggg gcc aac cga gaa ttt gat gaa aac aca	1365
Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr	
325 330 335	
tgc cag tgt gta tgt aaa aga acc tgc ccc aga aat caa ccc cta aat	1413
Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn	
340 345 350	
cct gga aaa tgt gcc tgt gaa tgt aca gaa agt cca cag aaa tgc ttg	1461
Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu	
355 360 365 370	
tta aaa gga aag aag ttc cac cac caa aca tgc agc tgt tac aga cgg	1509
Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg	
375 380 385	
cca tgt acg aac cgc cag aag gct tgt gag cca gga ttt tca tat agt	1557
Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser	
390 395 400	

caaaatatgt ttaaaataaa atgaaaattg tattat 1997

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<210> 24  
<211> 419  
<212> PRT  
<213> Homo sapiens
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<400> 24

Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
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Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe
20 25 30

Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
35 40 45

Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60

Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
65 70 75 80

Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
85 90 95

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
100 105 110

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
 145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
 165 170 175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
 180 185 190

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
 195 200 205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
 210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
 225 230 235 240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
 245 250 255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
 260 265 270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
 275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
 290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
 305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
 325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
 340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
 355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
 370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
 385 390 395 400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
 405 410 415

Gln Met Ser

<210> 25
 <211> 2029
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (411)..(1475)

<400> 25
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 aactagaacc tgcggcatatc attggagaga tttttttaat tttctggaca tgaagtaaatt 120
 ttagagtgtc ttctaatttc aggtagaaga catgtccacc ttctgattat ttttggagaa 180
 cattttgatt tttttcatct ctctctcccc acccctaaga ttgtgcaaaa aaagcgtacc 240
 ttgcctaatt gaaataattt cattggattt tgatcagaac tgattatttg gttttctgtg 300
 tgaagttttg aggtttcaaa ctttccttct ggagaatgcc ttttgaaaca attttctcta 360
 gctgcctgat gtcaactgct tagtaatcag tggatattga aatattcaaa atg tac 416
 Met Tyr
 1
 aga gag tgg gta gtg gtg aat gtt ttc atg atg ttg tac gtc cag ctg 464
 Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val Gln Leu
 5 10 15
 gtg cag ggc tcc agt aat gaa cat gga cca gtg aag cga tca tct cag 512
 Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser Ser Gln
 20 25 30
 tcc aca ttg gaa cga tct gaa cag cag atc agg gct gct tct agt ttg 560
 Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser Ser Leu
 35 40 45 50
 gag gaa cta ctt cga att act cac tct gag gac tgg aag ctg tgg aga 608
 Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu Trp Arg
 55 60 65
 tgc agg ctg agg ctc aaa agt ttt acc agt atg gac tct cgc tca gca 656
 Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg Ser Ala
 70 75 80
 tcc cat cgg tcc act agg ttt gcg gca act ttc tat gac att gaa aca 704
 Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile Glu Thr
 85 90 95
 cta aaa gtt ata gat gaa gaa tgg caa aga act cag tgc agc cct aga 752
 Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser Pro Arg
 100 105 110
 gaa acg tgc gtg gag gtg gcc agt gag ctg ggg aag agt acc aac aca 800
 Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr Asn Thr
 115 120 125 130

ttc ttc aag ccc cct tgt gtg aac gtg ttc cga tgt ggt ggc tgt tgc	848
Phe Phe Lys Pro Cys Val Asn Val Phe Arg Cys Gly Gly Cys Cys	
135 140 145	
aat gaa gag agc ctt atc tgt atg aac acc agc acc tcg tac att tcc	896
Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr Ile Ser	
150 155 160	
aaa cag ctc ttt gag ata tca gtg cct ttg aca tca gta cct gaa tta	944
Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro Glu Leu	
165 170 175	
gtg cct gtt aaa gtt gcc aat cat aca ggt tgt aag tgc ttg cca aca	992
Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu Pro Thr	
180 185 190	
gcc ccc cgc cat cca tac tca att atc aga aga tcc atc cag atc cct	1040
Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln Ile Pro	
195 200 205 210	
gaa gaa gat cgc tgt tcc cat tcc aag aaa ctc tgt cct att gac atg	1088
Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile Asp Met	
215 220 225	
cta tgg gat agc aac aaa tgt aaa tgt gtt ttg cag gag gaa aat cca	1136
Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu Asn Pro	
230 235 240	
ctt gct gga aca gaa gac cac tct cat ctc cag gaa cca gct ctc tgt	1184
Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala Leu Cys	
245 250 255	
ggg cca cac atg atg ttt gac gaa gat cgt tgc gag tgt gtc tgt aaa	1232
Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val Cys Lys	
260 265 270	
aca cca tgt ccc aaa gat cta atc cag cac ccc aaa aac tgc agt tgc	1280
Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys Ser Cys	
275 280 285 290	
ttt gag tgc aaa gaa agt ctg gag acc tgc tgc cag aag cac aag cta	1328
Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His Lys Leu	
295 300 305	
ttt cac cca gac acc tgc agc tgt gag gac aga tgc ccc ttt cat acc	1376
Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe His Thr	
310 315 320	
aga cca tgt gca agt ggc aaa aca gca tgt gca aag cat tgc cgc ttt	1424
Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys Arg Phe	
325 330 335	
cca aag gag aaa agg gct gcc cag ggg ccc cac agc cga aag aat cct	1472
Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys Asn Pro	
340 345 350	
tga ttcagcgttc caagttcccc atccctgtca tttttaacag catgctgctt	1525
tgccaagttg ctgtcactgt ttttttccca ggtgttaaaa aaaaaatcca ttttacacag	1585
caccacagtg aatccagacc aaccttccat tcacaccagc taaggagtcc ctggttcatt	1645

gatggatgtc ttctagctgc agatgcctct ggcaccaaag gaatggagag gaggggaccc 1705
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 catggaatgg caggtgtcat atgactgatt actcagagca gatgaggaaa actgtagtct 1825
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 tgattcgtat gatcagtact gactttctga ttactgtcca gcttatagtc ttccagttta 1945
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<210> 26

<211> 354

<212> PRT

<213> Homo sapiens

<400> 26

Met Tyr Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val
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20 25 30

Ser Gln Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
35 40 45

Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
50 55 60

Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
65 70 75 80

Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
85 90 95

Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
100 105 110

Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
115 120 125

Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
130 135 140

Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr
145 150 155 160

Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro
 165 170 175
 Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu
 180 185 190
 Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln
 195 200 205
 Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile
 210 215 220
 Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu
 225 230 235 240
 Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala
 245 250 255
 Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val
 260 265 270
 Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys
 275 280 285
 Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His
 290 295 300
 Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe
 305 310 315 320
 His Thr Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys
 325 330 335
 Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys
 340 345 350

Asn Pro

<210> 27
 <211> 1645
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (322)..(771)

<400> 27
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cccagccaca gccttaccta cgggctcctg actccgcaag gcttccagaa gatgctcgaa	180
ccaccgggccc gggcctcggg gcagcagtga gggaggcgct cagcccccca ctcagctctt	240
ctcctcctgt gccaggggct ccccggggga tgagcatggg ggttttccct cggagcccc	300
tggctcggga cgtctgagaa g atg ccg gtc atg agg ctg ttc cct tgc ttc	351
Met Pro Val Met Arg Leu Phe Pro Cys Phe	
1 5 10	
ctg cag ctc ctg gcc ggg ctg gcg ctg cct gct gtg ccc ccc cag cag	399
Leu Gln Leu Leu Ala Gly Leu Ala Leu Pro Ala Val Pro Pro Gln Gln	
15 20 25	
tgg gcc ttg tct gct ggg aac ggc tgc tca gag gtg gaa gtg gta ccc	447
Trp Ala Leu Ser Ala Gly Asn Gly Ser Ser Glu Val Glu Val Val Pro	
30 35 40	
ttc cag gaa gtg tgg ggc cgc agc tac tgc cgg gcg ctg gag agg ctg	495
Phe Gln Glu Val Trp Gly Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu	
45 50 55	
gtg gac gtc gtg tcc gag tac ccc agc gag gtg gag cac atg ttc agc	543
Val Asp Val Val Ser Glu Tyr Pro Ser Glu Val Glu His Met Phe Ser	
60 65 70	
cca tcc tgt gtc tcc ctg ctg cgc tgc acc ggc tgc tgc ggc gat gag	591
Pro Ser Cys Val Ser Leu Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu	
75 80 85 90	
aat ctg cac tgt gtg ccg gtg gag acg gcc aat gtc acc atg cag ctc	639
Asn Leu His Cys Val Pro Val Glu Thr Ala Asn Val Thr Met Gln Leu	
95 100 105	
cta aag atc cgt tct ggg gac cgg ccc tcc tac gtg gag ctg acg ttc	687
Leu Lys Ile Arg Ser Gly Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe	
110 115 120	
tct cag cac gtt cgc tgc gaa tgc cgg cct ctg cgg gag aag atg aag	735
Ser Gln His Val Arg Cys Glu Cys Arg Pro Leu Arg Glu Lys Met Lys	
125 130 135	
ccg gaa agg tgc ggc gat gct gtt ccc cgg agg taa cccaccctt	781
Pro Glu Arg Cys Gly Asp Ala Val Pro Arg Arg	
140 145	
ggaggagaga gaccccgcac ccggctcgtg tatttattac cgtcacactc ttcagtgact	841
cctgctggta cctgccctct atttattagc caactgtttc cctgctgaat gcctcgctcc	901
cttcaagacg aggggcaggg aaggacagga ccctcaggaa ttcagtgcct tcaacaacgt	961
gagagaaaga gagaagccag ccacagaccc ctgggagctt ccgctttgaa agaagcaaga	1021
cacgtggcct cgtgaggggc aagctaggcc ccagaggccc tggaggtctc caggggcctg	1081
cagaaggaaa gaagggggcc ctgctacctg ttcttgggcc tcaggctctg cacagacaag	1141
cagcccttgc ttccggagct cctgtccaaa gtagggatgc ggattctgct ggggccgcca	1201

cggcctggtg gtgggaaggc cggcagcggg cggaggggat tcagccactt cccctcttc 1261
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 ggaggagcct gtgcgtccca gctgaaggca gtggcagggg agcaggttcc ccaagggccc 1561
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 taaagtattc tagtgtggaa acgc 1645

<210> 28

<211> 149

<212> PRT

<213> Homo. sapiens

<400> 28

Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly
 1 5 10 15

Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly
 20 25 30

Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly
 35 40 45

Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu
 50 55 60

Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu
 65 70 75 80

Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro
 85 90 95

Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly
 100 105 110

Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys
 115 120 125

Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Cys Gly Asp
 130 135 140

Ala Val Pro Arg Arg
 145

<210> 29
 <211> 4230
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(4065)

<400> 29
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 Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu Thr Arg
 1 5 10 15
 gcc gcc tct gtg ggt ttg cct agt gtt tct ctt gat ctg ccc agg ctc 96
 Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro Arg Leu
 20 25 30
 agc ata caa aaa gac ata ctt aca att aag gct aat aca act ctt caa 144
 Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr Leu Gln
 35 40 45
 att act tgc agg gga cag agg gac ttg gac tgg ctt tgg ccc aat aat 192
 Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Asn
 50 55 60
 cag agt ggc agt gag caa agg gtg gag gtg act gag tgc agc gat ggc 240
 Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser Asp Gly
 65 70 75 80
 ctc ttc tgt aag aca ctc aca att cca aaa gtg atc gga aat gac act 288
 Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn Asp Thr
 85 90 95
 gga gcc tac aag tgc ttc tac cgg gaa act gac ttg gcc tcg gtc att 336
 Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser Val Ile
 100 105 110
 tat gtc tat gtt caa gat tac aga tct cca ttt att gct tct gtt agt 384
 Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val Ser
 115 120 125
 gac caa cat gga gtc gtg tac att act gag aac aaa aac aaa act gtg 432
 Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr Val
 130 135 140
 gtg att cca tgt ctc ggg tcc att tca aat ctc aac gtg tca ctt tgt 480
 Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser Leu Cys
 145 150 155 160
 gca aga tac cca gaa aag aga ttt gtt cct gat ggt aac aga att tcc 528
 Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile Ser
 165 170 175
 tgg gac agc aag aag ggc ttt act att ccc agc tac atg atc agc tat 576
 Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile Ser Tyr
 180 185 190
 gct ggc atg gtc ttc tgt gaa gca aaa att aat gat gaa agt tac cag 624
 Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser Tyr Gln
 195 200 205

tct att atg tac ata gtt gtc gtt gta ggg tat agg att tat gat gtg Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr Asp Val 210 215 220	672
gtt ctg agt ccg tct cat gga att gaa cta tct gtt gga gaa aag ctt Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu 225 230 235 240	720
gtc tta aat tgt aca gca aga act gaa cta aat gtg ggg att gac ttc Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe 245 250 255	768
aac tgg gaa tac cct tct tcg aag cat cag cat aag aaa ctt gta aac Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val Asn 260 265 270	816
cga gac cta aaa acc cag tct ggg agt gag atg aag aaa ttt ttg agc Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser 275 280 285	864
acc tta act ata gat ggt gta acc cgg agt gac caa gga ttg tac acc Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr 290 295 300	912
tgt gca gca tcc agt ggg ctg atg acc aag aag aac agc aca ttt gtc Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val 305 310 315 320	960
agg gtc cat gaa aaa cct ttt gtt gct ttt gga agt ggc atg gaa tct Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met Glu Ser 325 330 335	1008
ctg gtg gaa gcc acg gtg ggg gag cgt gtc aga atc cct gcg aag tac Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala Lys Tyr 340 345 350	1056
ctt ggt tac cca ccc cca gaa ata aaa tgg tat aaa aat gga ata ccc Leu Gly Tyr Pro Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly Ile Pro 355 360 365	1104
ctt gag tcc aat cac aca att aaa gcg ggg cat gta ctg acg att atg Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr Ile Met 370 375 380	1152
gaa gtg agt gaa aga gac aca gga aat tac act gtc atc ctt acc aat Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu Thr Asn 385 390 395 400	1200
ccc att tca aag gag aag cag agc cat gtg gtc tct ctg gtt gtg tat Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val Val Tyr 405 410 415	1248
gtc cca ccc cag att ggt gag aaa tct cta atc tct cct gtg gat tcc Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val Asp Ser 420 425 430	1296
tac cag tac ggc acc act caa acg ctg aca tgt acg gtc tat gcc att Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr Ala Ile 435 440 445	1344
cct ccc ccg cat cac atc cac tgg tat tgg cag ttg gag gaa gag tgc Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu Glu Cys 450 455 460	1392

gcc aac gag ccc agc caa gct gtc tca gtg aca aac cca tac cct tgt Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr Pro Cys 465 470 475 480	1440
gaa gaa tgg aga agt gtg gag gac ttc cag gga gga aat aaa att gaa Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu 485 490 495	1488
gtt aat aaa aat caa ttt gct cta att gaa gga aaa aac aaa act gta Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys Thr Val 500 505 510	1536
agt acc ctt gtt atc caa gcg gca aat gtg tca gct ttg tac aaa tgt Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys 515 520 525	1584
gaa gcg gtc aac aaa gtc ggg aga gga gag agg gtg atc tcc ttc cac Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser Phe His 530 535 540	1632
gtg acc agg ggt cct gaa att act ttg caa cct gac atg cag ccc act Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln Pro Thr 545 550 555 560	1680
gag cag gag agc gtg tct ttg tgg tgc act gca gac aga tct acg ttt Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser Thr Phe 565 570 575	1728
gag aac ctc aca tgg tac aag ctt ggc cca cag cct ctg cca atc cat Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro Ile His 580 585 590	1776
gtg gga gag ttg ccc aca cct gtt tgc aag aac ttg gat act ctt tgg Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr Leu Trp 595 600 605	1824
aaa ttg aat gcc acc atg ttc tct aat agc aca aat gac att ttg atc Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile 610 615 620	1872
atg gag ctt aag aat gca tcc ttg cag gac caa gga gac tat gtc tgc Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys 625 630 635 640	1920
ctt gct caa gac agg aag acc aag aaa aga cat tgc gtg gtc agg cag Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val Arg Gln 645 650 655	1968
ctc aca gtc cta gag cgt gtg gca ccc acg atc aca gga aac ctg gag Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn Leu Glu 660 665 670	2016
aat cag acg aca agt att ggg gaa agc atc gaa gtc tca tgc acg gca Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys Thr Ala 675 680 685	2064
tct ggg aat ccc cct cca cag atc atg ttg ttt aaa gat aat gag acc Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn Glu Thr 690 695 700	2112
ctt gta gaa gac tca ggc att gta ttg aag gat ggg aac cgg aac ctc Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg Asn Leu 705 710 715 720	2160

act atc cgc aga gtg agg aag gag gac gaa ggc ctc tac acc tgc cag Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr Cys Gln 725 730 735	2208
gca tgc agt gtt ctt ggc tgt gca aaa gtg gag gca ttt ttc ata ata Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe Ile Ile 740 745 750	2256
gaa ggt gcc cag gaa aag acg aac ttg gaa atc att att cta gta ggc Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu Val Gly 755 760 765	2304
acg acg gtg att gcc atg ttc ttc tgg cta ctt ctt gtc atc atc cta Thr Thr Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile Ile Leu 770 775 780	2352
ggg acc gtt aag cgg gcc aat gga ggg gaa ctg aag aca ggc tac ttg Gly Thr Val Lys Arg Ala Asn Gly Gly Glu Leu Lys Thr Gly Tyr Leu 785 790 795 800	2400
tcc atc gtc atg gat cca gat gaa ctc cca ttg gat gaa cat tgt gaa Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu His Cys Glu 805 810 815	2448
cga ctg cct tat gat gcc agc aaa tgg gaa ttc ccc aga gac cgg ctg Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp Arg Leu 820 825 830	2496
aac cta ggt aag cct ctt ggc cgt ggt gcc ttt ggc caa gag att gaa Asn Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Glu Ile Glu 835 840 845	2544
gca gat gcc ttt gga att gac aag aca gca act tgc agg aca gta gca Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr Val Ala 850 855 860	2592
gtc aaa atg ttg aaa gaa gga gca aca cac agt gag cat cga gct ctc Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu 865 870 875 880	2640
atg tct gaa ctc aag atc ctc att cat att ggt cac cat ctc aat gtg Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu Asn Val 885 890 895	2688
gtc aac ctt cta ggt gcc tgt acc aag cca gga ggg cca ctc atg gtg Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val 900 905 910	2736
att gtg gaa ttc tgc aaa ttt gga aac ctg tcc act tac ctg agg agc Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Ser 915 920 925	2784
aag aga aat gaa ttt gtc ccc tac aag acc aaa ggg gca cga ttc cgt Lys Arg Asn Glu Phe Val Pro Tyr Lys Thr Lys Gly Ala Arg Phe Arg 930 935 940	2832
caa ggg aaa gac tac gtt gga gca atc cct gtg gat ctg aaa cgg cgc Gln Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu Lys Arg Arg 945 950 955 960	2880
ttg gac agc atc acc agt agc cag agc tca gcc agc tct gga ttt gtg Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly Phe Val 965 970 975	2928

gag gag aag tcc ctc agt gat gta gaa gaa gag gaa gct cct gaa gat Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Ala Pro Glu Asp 980 985 990	2976
ctg tat aag gac ttc ctg acc ttg gag cat ctc atc tgt tac agc ttc Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr Ser Phe 995 1000 1005	3024
caa gtg gct aag ggc atg gag ttc ttg gca tcg cga aag tgt atc Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile 1010 1015 1020	3069
cac agg gac ctg gcg gca cga aat atc ctc tta tcg gag aag aac His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn 1025 1030 1035	3114
gtg gtt aaa atc tgt gac ttt ggc ttg gcc cgg gat att tat aaa Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys 1040 1045 1050	3159
gat cca gat tat gtc aga aaa gga gat gct cgc ctc cct ttg aaa Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu Lys 1055 1060 1065	3204
tgg atg gcc cca gaa aca att ttt gac aga gtg tac aca atc cag Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln 1070 1075 1080	3249
agt gac gtc tgg tct ttt ggt gtt ttg ctg tgg gaa ata ttt tcc Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Ser 1085 1090 1095	3294
tta ggt gct tct cca tat cct ggg gta aag att gat gaa gaa ttt Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe 1100 1105 1110	3339
tgt agg cga ttg aaa gaa gga act aga atg agg gcc cct gat tat Cys Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr 1115 1120 1125	3384
act aca cca gaa atg tac cag acc atg ctg gac tgc tgg cac ggg Thr Thr Pro Glu Met Tyr Gln Thr Met Leu Asp Cys Trp His Gly 1130 1135 1140	3429
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 Glu Leu Val Glu Ile Leu Gly Asp Leu Leu Gln Gly Arg Gly Leu Gln
 1165 1170 1175
 gag gaa gag gag gtc tgc atg gcc ccg cgc agc tct cag agc tca gaa 3604
 Glu Glu Glu Glu Val Cys Met Ala Pro Arg Ser Ser Gln Ser Ser Glu
 1180 1185 1190 1195
 gag ggc agc ttc tgc cag gtg tcc acc atg gcc cta cac atc gcc cag 3652
 Glu Gly Ser Phe Ser Gln Val Ser Thr Met Ala Leu His Ile Ala Gln
 1200 1205 1210
 gct gac gct gag gac agc ccg cca agc ctg cag cgc cac agc ctg gcc 3700
 Ala Asp Ala Glu Asp Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala
 1215 1220 1225
 gcc agg tat tac aac tgg gtg tcc ttt ccc ggg tgc ctg gcc aga ggg 3748
 Ala Arg Tyr Tyr Asn Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly
 1230 1235 1240
 gct gag acc cgt ggt tcc tcc agg atg aag aca ttt gag gaa ttc ccc 3796
 Ala Glu Thr Arg Gly Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro
 1245 1250 1255
 atg acc cca acg acc tac aaa ggc tct gtg gac aac cag aca gac agt 3844
 Met Thr Pro Thr Thr Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser
 1260 1265 1270 1275
 ggg atg gtg ctg gcc tgc gag gag ttt gag cag ata gag agc agg cat 3892
 Gly Met Val Leu Ala Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His
 1280 1285 1290
 aga caa gaa agc ggc ttc agg tagctgaagc agagagagag aaggcagcat 3943
 Arg Gln Glu Ser Gly Phe Arg
 1295
 acgtcagcat tttcttctct gcacttataa gaaagatcaa agactttaag actttcgcta 4003
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 gaaagtggac aaggagtgtg accactgaag caccacaggg aaggggttag gcctccggat 4123
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 tccctgactc ct 4195

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 <211> 1298
 <212> PRT
 <213> Homo sapiens

<400> 32
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Asn Ile Thr Glu Glu Ser His Val Ile Asp Thr Gly Asp Ser Leu Ser
 35 40 45

Ile Ser Cys Arg Gly Gln His Pro Leu Glu Trp Ala Trp Pro Gly Ala
 50 55 60

Gln Glu Ala Pro Ala Thr Gly Asp Lys Asp Ser Glu Asp Thr Gly Val
 65 70 75 80

Val Arg Asp Cys Glu Gly Thr Asp Ala Arg Pro Tyr Cys Lys Val Leu
 85 90 95

Leu Leu His Glu Val His Ala Asn Asp Thr Gly Ser Tyr Val Cys Tyr
 100 105 110

Tyr Lys Tyr Ile Lys Ala Arg Ile Glu Gly Thr Thr Ala Ala Ser Ser
 115 120 125

Tyr Val Phe Val Arg Asp Phe Glu Gln Pro Phe Ile Asn Lys Pro Asp
 130 135 140

Thr Leu Leu Val Asn Arg Lys Asp Ala Met Trp Val Pro Cys Leu Val
 145 150 155 160

Ser Ile Pro Gly Leu Asn Val Thr Leu Arg Ser Gln Ser Ser Val Leu
 165 170 175

Trp Pro Asp Gly Gln Glu Val Val Trp Asp Asp Arg Arg Gly Met Leu
 180 185 190

Val Ser Thr Pro Leu Leu His Asp Ala Leu Tyr Leu Gln Cys Glu Thr
 195 200 205

Thr Trp Gly Asp Gln Asp Phe Leu Ser Asn Pro Phe Leu Val His Ile
 210 215 220

Thr Gly Asn Glu Leu Tyr Asp Ile Gln Leu Leu Pro Arg Lys Ser Leu
 225 230 235 240

Glu Leu Leu Val Gly Glu Lys Leu Val Leu Asn Cys Thr Val Trp Ala
 245 250 255

Glu Phe Asn Ser Gly Val Thr Phe Asp Trp Asp Tyr Pro Gly Lys Gln
 260 265 270

Ala Glu Arg Gly Lys Trp Val Pro Glu Arg Arg Ser Gln Gln Thr His
 275 280 285

Thr Glu Leu Ser Ser Ile Leu Thr Ile His Asn Val Ser Gln His Asp
 290 295 300

Leu Gly Ser Tyr Val Cys Lys Ala Asn Asn Gly Ile Gln Arg Phe Arg
 305 310 315 320

Glu Ser Thr Glu Val Ile Val His Glu Asn Pro Phe Ile Ser Val Glu
 325 330 335

Trp Leu Lys Gly Pro Ile Leu Glu Ala Thr Ala Gly Asp Glu Leu Val
 340 345 350

Lys Leu Pro Val Lys Leu Ala Ala Tyr Pro Pro Pro Glu Phe Gln Trp
 355 360 365

Tyr Lys Asp Gly Lys Ala Leu Ser Gly Arg His Ser Pro His Ala Leu
 370 375 380

Val Leu Lys Glu Val Thr Glu Ala Ser Thr Gly Thr Tyr Thr Leu Ala
 385 390 395 400

Leu Trp Asn Ser Ala Ala Gly Leu Arg Arg Asn Ile Ser Leu Glu Leu
 405 410 415

Val Val Asn Val Pro Pro Gln Ile His Glu Lys Glu Ala Ser Ser Pro
 420 425 430

Ser Ile Tyr Ser Arg His Ser Arg Gln Ala Leu Thr Cys Thr Ala Tyr
 435 440 445

Gly Val Pro Leu Pro Leu Ser Ile Gln Trp His Trp Arg Pro Trp Thr
 450 455 460

Pro Cys Lys Met Phe Ala Gln Arg Ser Leu Arg Arg Arg Gln Gln Gln
 465 470 475 480

Asp Leu Met Pro Gln Cys Arg Asp Trp Arg Ala Val Thr Thr Gln Asp
 485 490 495

Ala Val Asn Pro Ile Glu Ser Leu Asp Thr Trp Thr Glu Phe Val Glu
 500 505 510

Gly Lys Asn Lys Thr Val Ser Lys Leu Val Ile Gln Asn Ala Asn Val
 515 520 525

Ser Ala Met Tyr Lys Cys Val Val Ser Asn Lys Val Gly Gln Asp Glu
 530 535 540

Arg Leu Ile Tyr Phe Tyr Val Thr Thr Ile Pro Asp Gly Phe Thr Ile
 545 550 555 560

Glu Ser Lys Pro Ser Glu Glu Leu Leu Glu Gly Gln Pro Val Leu Leu
 565 570 575

Ser Cys Gln Ala Asp Ser Tyr Lys Tyr Glu His Leu Arg Trp Tyr Arg
 580 585 590

Leu Asn Leu Ser Thr Leu His Asp Ala His Gly Asn Pro Leu Leu Leu
 595 600 605

Asp Cys Lys Asn Val His Leu Phe Ala Thr Pro Leu Ala Ala Ser Leu
 610 615 620

Glu Glu Val Ala Pro Gly Ala Arg His Ala Thr Leu Ser Leu Ser Ile
 625 630 635 640

Pro Arg Val Ala Pro Glu His Glu Gly His Tyr Val Cys Glu Val Gln
 645 650 655

Asp Arg Arg Ser His Asp Lys His Cys His Lys Lys Tyr Leu Ser Val
 660 665 670

Gln Ala Leu Glu Ala Pro Arg Leu Thr Gln Asn Leu Thr Asp Leu Leu
 675 680 685

Val Asn Val Ser Asp Ser Leu Glu Met Gln Cys Leu Val Ala Gly Ala
 690 695 700

His Ala Pro Ser Ile Val Trp Tyr Lys Asp Glu Arg Leu Leu Glu Glu
 705 710 715 720

Lys Ser Gly Val Asp Leu Ala Asp Ser Asn Gln Lys Leu Ser Ile Gln
 725 730 735

Arg Val Arg Glu Glu Asp Ala Gly Arg Tyr Leu Cys Ser Val Cys Asn
 740 745 750

Ala Lys Gly Cys Val Asn Ser Ser Ala Ser Val Ala Val Glu Gly Ser
 755 760 765

Glu Asp Lys Gly Ser Met Glu Ile Val Ile Leu Val Gly Thr Gly Val
 770 775 780

Ile Ala Val Phe Phe Trp Val Leu Leu Leu Leu Ile Phe Cys Asn Met
 785 790 795 800

Arg Arg Pro Ala His Ala Asp Ile Lys Thr Gly Tyr Leu Ser Ile Ile
 805 810 815

Met Asp Pro Gly Glu Val Pro Leu Glu Glu Gln Cys Glu Tyr Leu Ser
 820 825 830

Tyr Asp Ala Ser Gln Trp Glu Phe Pro Arg Glu Arg Leu His Leu Gly
 835 840 845

Arg Val Leu Gly Tyr Gly Ala Phe Gly Lys Val Val Glu Ala Ser Ala
 850 855 860

Phe Gly Ile His Lys Gly Ser Ser Cys Asp Thr Val Ala Val Lys Met
 865 870 875 880

Leu Lys Glu Gly Ala Thr Ala Ser Glu His Arg Ala Leu Met Ser Glu
 885 890 895

Leu Lys Ile Leu Ile His Ile Gly Asn His Leu Asn Val Val Asn Leu
 900 905 910

Leu Gly Ala Cys Thr Lys Pro Gln Gly Pro Leu Met Val Ile Val Glu
 915 920 925

Phe Cys Lys Tyr Gly Asn Leu Ser Asn Phe Leu Arg Ala Lys Arg Asp
 930 935 940

Ala Phe Ser Pro Cys Ala Glu Lys Ser Pro Glu Gln Arg Gly Arg Phe
 945 950 955 960

Arg Ala Met Val Glu Leu Ala Arg Leu Asp Arg Arg Arg Pro Gly Ser
 965 970 975

Ser Asp Arg Val Leu Phe Ala Arg Phe Ser Lys Thr Glu Gly Gly Ala
 980 985 990

Arg Arg Ala Ser Pro Asp Gln Glu Ala Glu Asp Leu Trp Leu Ser Pro
 995 1000 1005

Leu Thr Met Glu Asp Leu Val Cys Tyr Ser Phe Gln Val Ala Arg Gly
 1010 1015 1020

Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala
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Arg Asn Ile Leu Leu Ser Glu Ser Asp Val Val Lys Ile Cys Asp Phe

1045	1050	1055
Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly 1060 1065 1070		
Ser Ala Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asp 1075 1080 1085		
Lys Val Tyr Thr Thr Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu 1090 1095 1100		
Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Gln Ile 1105 1110 1115 1120		
Asn Glu Glu Phe Cys Gln Arg Leu Arg Asp Gly Thr Arg Met Arg Ala 1125 1130 1135		
Pro Glu Leu Ala Thr Pro Ala Ile Arg Arg Ile Met Leu Asn Cys Trp 1140 1145 1150		
Ser Gly Asp Pro Lys Ala Arg Pro Ala Phe Ser Glu Leu Val Glu Ile 1155 1160 1165		
Leu Gly Asp Leu Leu Gln Gly Arg Gly Leu Gln Glu Glu Glu Glu Val 1170 1175 1180		
Cys Met Ala Pro Arg Ser Ser Gln Ser Ser Glu Glu Gly Ser Phe Ser 1185 1190 1195 1200		
Gln Val Ser Thr Met Ala Leu His Ile Ala Gln Ala Asp Ala Glu Asp 1205 1210 1215		
Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala Ala Arg Tyr Tyr Asn 1220 1225 1230		
Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly Ala Glu Thr Arg Gly 1235 1240 1245		
Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro Met Thr Pro Thr Thr 1250 1255 1260		
Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala 1265 1270 1275 1280		
Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His Arg Gln Glu Ser Gly 1285 1290 1295		

Phe Arg

<210> 33
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 <212> PRT
 <213> Homo sapiens

<400> 33

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
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<210> 34
 <211> 18
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic primer

<400> 34
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<210> 35
 <211> 18
 <212> DNA
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<220>
 <223> Synthetic primer

<400> 35
 aagttgggta acgccagg 18

<210> 36
 <211> 15
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic primer

<400> 36
 tgacctcgcc cccgt 15

<210> 37
 <211> 3088
 <212> DNA
 <213> Homo sapiens

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 tgaatcataa taaaatagcc tctaaacagt ttctaagcgg gagcctccgt ggaactcagc 180
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cttattcggg aagtgcaatg caggaaggat tgtcacccaa tcacttgaaa aaagcaaagc	2040
tcatgttttt ttatacccgt tatcccagct ccaatatgct gaagacctac ttctccgacg	2100
taaagttcaa cagatgcatt acctctcagc tcatcaagtg gtttagcaat ttccgtgagt	2160

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aaccacttca tacatttaag tattttgttt ggtttgaact caatcagtag cttttcctta 3000
catgtttaaa aataattcca atgacagatg agcagctcac ttttccaaag taccocaaaa 3060
ggccaaatta aaaaaaaaaa aaaaaaaaaa 3088

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<210> 38

<211> 737

<212> PRT

<213> Homo sapiens

<400> 38

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Met Pro Asp His Asp Ser Thr Ala Leu Leu Ser Arg Gln Thr Lys Arg
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Arg Arg Val Asp Ile Gly Val Lys Arg Thr Val Gly Thr Ala Ser Ala
20          25          30

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Phe Phe Ala Lys Ala Arg Ala Thr Phe Phe Ser Ala Met Asn Pro Gln
35          40          45

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```

Gly Ser Glu Gln Asp Val Glu Tyr Ser Val Val Gln His Ala Asp Gly
50          55          60

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Glu Lys Ser Asn Val Leu Arg Lys Leu Leu Lys Arg Ala Asn Ser Tyr
65          70          75          80

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Glu Asp Ala Met Met Pro Phe Pro Gly Ala Thr Ile Ile Ser Gln Leu
85          90          95

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Leu Lys Asn Asn Met Asn Lys Asn Gly Gly Thr Glu Pro Ser Phe Gln
 100 105 110

Ala Ser Gly Leu Ser Ser Thr Gly Ser Glu Val His Gln Glu Asp Ile
 115 120 125

Cys Ser Asn Ser Ser Arg Asp Ser Pro Pro Glu Cys Leu Ser Pro Phe
 130 135 140

Gly Arg Pro Thr Met Ser Gln Phe Asp Met Asp Arg Leu Cys Asp Glu
 145 150 155 160

His Leu Arg Ala Lys Arg Ala Arg Val Glu Asn Ile Ile Arg Gly Met
 165 170 175

Ser His Ser Pro Ser Val Ala Leu Arg Gly Asn Glu Asn Glu Arg Glu
 180 185 190

Met Ala Pro Gln Ser Val Ser Pro Arg Glu Ser Tyr Arg Glu Asn Lys
 195 200 205

Arg Lys Gln Lys Leu Pro Gln Gln Gln Gln Gln Ser Phe Gln Gln Leu
 210 215 220

Val Ser Ala Arg Lys Glu Gln Lys Arg Glu Glu Arg Arg Gln Leu Lys
 225 230 235 240

Gln Gln Leu Glu Asp Met Gln Lys Gln Leu Arg Gln Leu Gln Glu Lys
 245 250 255

Phe Tyr Gln Ile Tyr Asp Ser Thr Asp Ser Glu Asn Asp Glu Asp Gly
 260 265 270

Asn Leu Ser Glu Asp Ser Met Arg Ser Glu Ile Leu Asp Ala Arg Ala
 275 280 285

Gln Asp Ser Val Gly Arg Ser Asp Asn Glu Met Cys Glu Leu Asp Pro
 290 295 300

Gly Gln Phe Ile Asp Arg Ala Arg Ala Leu Ile Arg Glu Gln Glu Met
 305 310 315 320

Ala Glu Asn Lys Pro Lys Arg Glu Gly Asn Asn Lys Glu Arg Asp His
 325 330 335

Gly Pro Asn Ser Leu Gln Pro Glu Gly Lys His Leu Ala Glu Thr Leu
 340 345 350

Lys Gln Glu Leu Asn Thr Ala Met Ser Gln Val Val Asp Thr Val Val
 355 360 365

Lys Val Phe Ser Ala Lys Pro Ser Arg Gln Val Pro Gln Val Phe Pro
 370 375 380

Pro Leu Gln Ile Pro Gln Ala Arg Phe Ala Val Asn Gly Glu Asn His
 385 390 395 400

Asn Phe His Thr Ala Asn Gln Arg Leu Gln Cys Phe Gly Asp Val Ile
 405 410 415

Ile Pro Asn Pro Leu Asp Thr Phe Gly Asn Val Gln Met Ala Ser Ser
 420 425 430

Thr Asp Gln Thr Glu Ala Leu Pro Leu Val Val Arg Lys Asn Ser Ser
 435 440 445

Asp Gln Ser Ala Ser Gly Pro Ala Ala Gly Gly His His Gln Pro Leu
 450 455 460

His Gln Ser Pro Leu Ser Ala Thr Thr Gly Phe Thr Thr Ser Thr Phe
 465 470 475 480

Arg His Pro Phe Pro Leu Pro Leu Met Ala Tyr Pro Phe Gln Ser Pro
 485 490 495

Leu Gly Ala Pro Ser Gly Ser Phe Ser Gly Lys Asp Arg Ala Ser Pro
 500 505 510

Glu Ser Leu Asp Leu Thr Arg Asp Thr Thr Ser Leu Arg Thr Lys Met
 515 520 525

Ser Ser His His Leu Ser His His Pro Cys Ser Pro Ala His Pro Pro
 530 535 540

Ser Thr Ala Glu Gly Leu Ser Leu Ser Leu Ile Lys Ser Glu Cys Gly
 545 550 555 560

Asp Leu Gln Asp Met Ser Glu Ile Ser Pro Tyr Ser Gly Ser Ala Met
 565 570 575

Gln Glu Gly Leu Ser Pro Asn His Leu Lys Lys Ala Lys Leu Met Phe
 580 585 590

Phe Tyr Thr Arg Tyr Pro Ser Ser Asn Met Leu Lys Thr Tyr Phe Ser
 595 600 605

Asp Val Lys Phe Asn Arg Cys Ile Thr Ser Gln Leu Ile Lys Trp Phe
 610 615 620

Ser Asn Phe Arg Glu Phe Tyr Tyr Ile Gln Met Glu Lys Tyr Ala Arg
 625 630 635 640

Gln Ala Ile Asn Asp Gly Val Thr Ser Thr Glu Glu Leu Ser Ile Thr
 645 650 655

Arg Asp Cys Glu Leu Tyr Arg Ala Leu Asn Met His Tyr Asn Lys Ala
 660 665 670

Asn Asp Phe Glu Val Pro Glu Arg Phe Leu Glu Val Ala Gln Ile Thr
 675 680 685

Leu Arg Glu Phe Phe Asn Ala Ile Ile Ala Gly Lys Asp Val Asp Pro
 690 695 700

Ser Trp Lys Lys Ala Ile Tyr Lys Val Ile Cys Lys Leu Asp Ser Glu
 705 710 715 720

Val Pro Glu Ile Phe Lys Ser Pro Asn Cys Leu Gln Glu Leu Leu His
 725 730 735

Glu